

IN THE CLAIMS

This listing of the claims will replace all prior versions, and listings, of the claims in the application.

1 – 5. (Cancelled)

6. (Previously presented) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation providing means for improving functionality of the variant cellobiohydrolase with respect to the wild-type cellobiohydrolase.

7. (Currently amended) The nucleic acid molecule of claim 6 wherein the means for improving ~~is selected from the group consisting of~~ comprises

(a) ~~proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;~~

(b) ~~a helix capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;~~

(c) ~~substitution of glycine at position 99;~~

(d) ~~a substitution of cysteine at positions 197 and 370;~~

(e) ~~substitution of a non-glycosyl-accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof;~~

(f) ~~alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and~~

~~(g) any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase of SEQ ID NO: 5.~~

8. (Cancelled)

9. (Withdrawn) The nucleic acid molecule of claim 7 wherein the means for improving comprises the helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position **64, 337, 327, 405, 410** and any combination thereof.

10. (Withdrawn) The nucleic acid molecule of claim **7** wherein the means for improving comprises substitution of glycine at position 99.

11. (Currently amended) A method for mutating a nucleic acid encoding a wild type cellobiohydrolase of SEQ ID NO: 5, the method comprising:

mutating the wild type cellobiohydrolase with ~~a mutation selected from the group consisting of:~~

~~(a) proline substituted at a position selected from the group consisting of position 8; 37, 43, 76, 94, 190, 195, 197, 322, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;~~

~~(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;~~

~~(c) substitution of glycine at position 99;~~

~~(d) a substitution of cysteine at positions 197 and 370;~~

~~(e) substitution of a non-glycosyl-accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof;~~

~~(f) alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and~~

~~(g) any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild type cellobiohydrolase of SEQ ID NO: 5.~~

12. (Withdrawn) The method of claim 11, wherein the mutation comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

13. (Previously presented) The method of claims 11, wherein the step of mutating comprises site-directed mutagenesis.

14. (Previously presented) The method of claim 11, further comprising a step of shortening a linker region of the wild-type cellobiohydrolase with respect to wild-type linker region SEQ ID NO: 2 to provide a linker region having a length of from about 6 amino acids to about 17 amino acids located, between a catalytic domain and a cellulose binding domain (CBD) of SEQ ID NO: 5.

15. (Withdrawn) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 71.

16. (Withdrawn) **An** exoglucanase, comprising the sequence change encoded by SEQ ID NO: 74.

17 – 19. (Cancelled).

20. (Withdrawn) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a cysteine at positions 197 and 370.

21. (Withdrawn) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

22. (Withdrawn) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of an alanine at a position selected from the group consisting of position 45, 270, 384 any combination thereof.

23. (Cancelled).

24. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises means for enhancing thermostability.

25. (Currently amended) The nucleic acid molecule of claim 6, wherein the variant cellobiohydrolase comprises a linker region having a length of from about 6 amino acids to about 17 amino acids located between a catalytic domain and a cellulose binding domain (CBD) and wherein the variant cellobiohydrolase comprises a proline substituted at position 8 relative to SEQ ID NO: 5.

26. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation ~~selected from the group consisting of~~ comprising

- (a) ~~proline substituted at a position selected from the group consisting of position 89, 27, 122, 155, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 133, and any combination thereof;~~
- (b) ~~a helix capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;~~
- (c) ~~substitution of glycine at position 99;~~
- (d) ~~a substitution of cysteine at positions 197 and 370;~~
- (e) ~~substitution of a non-glycosyl-accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 684 and any combination thereof;~~
- (f) ~~alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and~~
- (g) ~~any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase SEQ ID NO: 5.~~

27. (Withdrawn) **An** exoglucanase, comprising the sequence change encoded by SEQ **ID NO:77**.

28. (Withdrawn) An exoglucanase composition, comprising a combination of exoglucanases selected from the group consisting of exoglucanases defined by claims 15, 16 and 27.

29. (New) The nucleic acid molecule of claim 6 wherein the means for improving functionality comprises means for enhancing thermostability.

30. (New) The nucleic acid molecule of claim 26, wherein the variant cellobiohydrolase is further mutated with a mutation selected from the group consisting of:

- (a) proline substituted at a position selected from the group consisting of position 9, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;
- (b) a helix-capping mutation defined as an arginine or aspartic acid residue substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;
- (c) substitution of glycine at position 99;
- (d) substitution of cysteine at positions 197 and 370;
- (e) substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 684 and any combination thereof,
- (f)** alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and
- (g) any combination of the mutations of (a), (b), (c), (d), (e), **(f)**, wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase SEQ ID NO: 5.